



# **STIC Search Report**

## **Biotech-Chem Library**

### **STIC Database Tracking Number**

**TO: Terra Gibbs**  
**Location: CM1/12A12/11E12**  
**Art Unit: 1635**  
**Thursday, June 19, 2003**

**Case Serial Number: 998667**

**From: Mary Jane Ruhl**  
**Location: Biotech-Chem Library**  
**CM1-6A06**  
**Phone: 605-1155**

**maryjane.ruhl@uspto.gov**

### **Search Notes**



**From:** Gibbs, Terra  
**Sent:** Wednesday, June 18, 2003 12:45 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** Sequence search request...

96916

Could you please do a regular search of SEQ ID NO: 1 of USSN 09/998667?

Thank You!

**Terra Gibbs**  
**AU 1635**  
**306-3221**  
**Mailbox: 11E12**

CFE

Mary Jane Ruhl  
Tech. Info. Specialist, STIC  
TC-1600  
CM-1, Room 6A-06  
Phone: 605-1155



GenCore version 5.1.6

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us protein - protein search, using SW model

run on:

June 18, 2003, 17:27:18, Search time 70 Seconds

(without alignments)

File:

Sequence:

US-09-998-667-1

441,631 Million Cell updates/sec

Score:

1.257

1 MSVS:STDSCRAFAAATAR.....LIRRLDLSLEYVNSHTI 232

Score and table:

Gapop: 10.0, Gapext: 0.5

Search:

Gapop: 10.0, Gapext: 0.5

Total number of hits satisfying chosen parameters:

908470

Minimum hit seq length: 0

Maximum hit seq length: 2000000000

Post processing:

Minimum Match: 0.3

Maximum Match: 0.3

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## SUMMARIES

Prod. No. 18 The number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	Description
1	1.252	99.6	232	22	AA040028 Human polypeptide
2	1.19	73.1	185	22	AA010914 Human gene 6 clone
3	1.15	62.9	156	21	AA040398 Human GREF 048176
4	1.14	62.9	156	21	AA040398 Human polypeptide
5	1.13	62.9	156	21	AA040398 Novel human protein
6	1.12	62.9	156	21	Human gene 6 clone
7	1.11	62.9	156	21	Human novel 18 cDNA
8	1.10	62.9	156	21	Human collagen 10
9	1.09	62.9	156	21	Human novel gene
10	1.08	62.9	156	21	Mus myosin 10b





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 108 W41: 2000-587533/55.  
 109 N PSHB: AA78070.  
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 111 Novel isolated nucleic acids comprising sequences encoding peptides  
 112 useful for treating or diagnosing e.g. cancer -  
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[illegible]

17	NEW 2509	2509035-0249245	
18	NEW 2509	2509035-0249264	
19	NEW 2509	2509035-0249265	
20	NEW 2509	2509035-0249297	
21	NEW 2509	2509035-0249300	
22	NEW 2509	2509035-0249301	
23	NEW 2509	2509035-0251030	
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99	NEW 2509	2509035-0254678	
100	NEW 2509	2509035-0254678	







be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays (e.g., radioimmunoassays or enzyme-linked immunosorbent assays (ELISA)). Disorders which are diagnosed or treated include autoimmune diseases (e.g., rheumatoid arthritis, hyperthyroidism, diabetes mellitus, myelomas of the breast or liver, cardiovascular disorders (e.g., cardiac arrest), cerebrovascular disorders (e.g., cerebral ischemia), anemias, hemophias, neurological disorders (e.g., Alzheimer's disease), infections caused by bacteria, viruses and fungi and vascular disorders and neurological tumors, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain certain bacteria transplanted, for supporting cell culture of primary tissues, to regenerate tissues and in chemicals. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamin, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention.

Query Match	21.78	Score 27	10.4th 26
Best Local Similarity	28.98	Prod. No. 190040	
Match has	65	Character	91
	51	Mismatch	38
			100

Mathews 65, Culbertson 91, Muskat 91, Hodel 98

35 FIVEVY EVIWOVC TCVWV'CVT|A|CENNVIT|YIBAV|| SH.VP ALLX 879

[illegible][illegible][illegible][illegible]

1. The first part of the paper is devoted to the study of the properties of the function  $f(x) = \sum_{n=0}^{\infty} \frac{x^n}{n!}$  for  $x \in \mathbb{R}$ . It is shown that this function is the unique solution of the differential equation  $y' = y$  with the initial condition  $y(0) = 1$ . The function is also shown to be the limit of the partial sums of the series  $\sum_{n=0}^{\infty} \frac{x^n}{n!}$  as  $x \rightarrow \infty$ .

1 28 -----| (E) FTAAKV - - | (b) (b) V - F | (E) T | (H) S | (R) V | (E) R | 1 176

[illegible]

177 PDNPSFSSONLIRHLYSHITLFYQBITFNITFFALLIPEVLURS 221  
+ + + + +  
236 PWGHSQSILRNIVSHTNOHPEDVDEAVNLGLTFEYOYIAVEAS 280  
+ + + + +

RESOL 13  
AAM80029

1b AAM80029 standard; Protein: 133 AA

XX  
XX  
XX

AA80029;  
A  
XX

U(1)-N<sup>2</sup>V-2001 (first entry)

# XX

IDE. Human protein seq ID No 367%.

Human: cytokines; cell proliferation; cell differentiation; gene therapy;

kin vaccine, peptide therapy, stem cell growth factor; hematopoiesis;

[illegible]

Homo sapiens.

$$W_1(200) [57]^{40-A_2'}$$

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XX      Pang YL, Liu C, Drmanac RT, Asundi V, Zhou P, Xu G, Gao Y, Ma Y:
P1      Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW:
P1      Xue AJ, Yang Y, Wejman L, Goodrich R:
XX
XX      WPI: 2001-476283/51.
OR      N-PSDB: AAK53162.
XX
P1      Nucleic acids encoding polypeptides with cytokine like activities,
P1      useful in diagnosis and gene therapy.
P1      Claim 20: Page 410: 6221pp: Eng15th.
PS
XX
XX      The invention relates to polynucleotides (AAK51456-AAK53435) and the
C1      encoded polypeptides (AAK78423-AAK80402) that exhibit activity relating to
C1      cytokine, cell proliferation or cell differentiation or which may induce
C1      production of other cytokines in other cell populations. The
C1      polynucleotides and polypeptides are useful in gene therapy, vaccines or
C1      peptide therapy. The polypeptides have various cytokine like activities,
C1      e.g. stem cell growth factor activity, haematopoiesis regulating
C1      activity, tissue growth factor activity, immunomodulatory activity and
C1      activity/inhibit activity and may be useful in the diagnosis and/or
C1      treatment of cancer, leukemia, nervous system disorders, arthritis and
C1      inflammation.
C1      Note: Figures 1-9, 21-213 (AAK5281), 214 (AAK5282) and 300-
C1      (AAK80402) are omitted as the relevant pages from the sequence listing
C1      were missing at the time of publication.
XX
SQ      Sequence: 133 AA:

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Query Match: 16.2%; Score 204; DB 22; Length 133;
Best Local Similarity: 32.4%; Prod. No. 1e-13;
Matches 46; Conservative 19; Mismatches 43; Indels 34; Gaps 3;

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QY      144 C-QRELYEDSLDHCITHRSEKRPVPGICRLIPFNPSSFGNLTPELQVSHLEFYD 202
DB      51 GGAKNLDQDELKCHVESHRSDRNVCPICSAMWGPSPYSKANFLQHLHRKRFSDY 110
QY      204 FTFNFTIEALTRVVDRELLR 224
DB      111 FVDYSIDEPAAFOALATSLSE 142

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Search completed: June 18, 2003, 17:29:08  
 Job time: 72 secs

Database version 5.1.9  
Copyright (c) 1993 - 2003 CompuGen, Ltd.

00M protein - protein search, using SW model

Run on: June 18, 2003, 17:27:22 : Search time 14 seconds

(without alignment)  
487,580 Million cell updates/sec

Title: US-09-998-667-1

Feature source: 1257

Sequence: 1 MSAVSTSTKSKSAASATAP : : LIPVLDRLLELVNHSNTT 232

Scoring table: BLAST62

Gapcp 10 0 , Gapext 0 5

Searched: 262574 seqs, 26425922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum hit seq length: 0  
Maximum hit seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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7: /seq2/6/pt/ab01/104/55A.COMB.pep.\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	db	Hit	Description
1	295	21.5	245	2	US-08-897-340-46	Sequence 36, Appl
2	295	21.5	245	4	US-09-252-329-46	Sequence 36, Appl
3	283	22.5	245	4	US-08-897-340-45	Sequence 35, Appl
4	283	22.5	245	4	US-09-252-329-45	Sequence 35, Appl
5	155.5	12.4	557	4	US-09-138-2770-3	Sequence 3, Appl
6	155	12.4	522	1	US-08-699-347-2	Sequence 2, Appl
7	155	12.4	522	1	US-08-975-405-2	Sequence 2, Appl
8	148.5	11.8	558	4	US-09-138-2770-1	Sequence 2, Appl
9	142.5	11.3	448	4	US-09-268-5448-46	Sequence 36, Appl
10	141.5	10.7	543	4	US-08-697-610-2	Sequence 2, Appl
11	141.5	10.7	543	4	US-09-349-557-2	Sequence 2, Appl
12	139	10.3	450	4	US-08-818-514-6	Sequence 6, Appl
13	139	10.3	450	4	US-09-115-934A-6	Sequence 6, Appl
14	125	9.9	100	4	US-09-270-196-5	Sequence 5, Appl
15	120	9.5	412	4	US-08-425-061-18	Sequence 18, Appl
16	120	9.5	412	4	US-08-825-886-18	Sequence 18, Appl
17	120	9.5	765	1	US-08-425-061-19	Sequence 19, Appl
18	120	9.5	765	2	US-08-825-886-19	Sequence 19, Appl
19	120	9.5	900	2	US-08-435-451-20	Sequence 20, Appl
20	120	9.5	900	2	US-08-825-886-20	Sequence 20, Appl
21	120	9.5	914	1	US-08-425-061-21	Sequence 21, Appl
22	120	9.5	914	1	US-08-825-886-21	Sequence 21, Appl
23	120	9.5	1040	2	US-08-254-989-2	Sequence 2, Appl
24	120	9.5	1202	2	US-08-425-061-22	Sequence 22, Appl
25	120	9.5	1202	2	US-08-825-886-22	Sequence 22, Appl
26	120	9.5	1463	4	US-09-074-475-4	Sequence 4, Appl
27	120	9.5	1463	4	US-09-074-475-4	Sequence 4, Appl
28	120	9.5	1463	2	US-08-825-886-23	Sequence 23, Appl

28	120	9.5	1462	1	US-08-425-061-24	Sequence 24, Appl
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38	120	9.5	1853	1	US-08-488-0118-2	Sequence 2, Appl
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44	120	9.5	1853	4	US-09-074-475-4	Sequence 4, Appl
45	120	9.5	1853	4	US-09-074-475-4	Sequence 4, Appl

#### ALIGNMENTS

##### RESULT 1

US-08-897-340-46  
Sequence 36, Application US-08/897,340

Patent No. 5955300

GENERAL INFORMATION:

APPLICANT: Glaxo, Carlos J. and Patricia, Patrick, R

TITLE OF INVENTION: Weight Control Pathway Genes and Uses

INVENTOR: Thorton

NUMBER OF SEQUENCES: 46

CORRESPONDING ADDRESS:

ADDRESS: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

COMPILED BY: 02/09

DB 16 FVAVLGVVLAIPVLAAGHVGZSLIAMPSSLLHCLGSSVILPFFAVCPFAH 75  
 87 IIYAKMSEGVNCAETILVCLSEPMALIEPOVYIDK 139  
 DB 76 FNMRFSSGSSCHVSKRLEKYPMPYPSYFYGLVGVSVLNFRLSGSVSSN 142  
 140 -----WCFQCOBELY-FDLSLDEITTHRSRRKVPQCH 174  
 DB 133 RSTSSASNTETVQELISSSHPTKPTLCCQESNFKORLLDHNSNHLVQIVYVPT 192  
 174 KIPNPSPSPSGNLIHQVSHIIFYDFIIPNFIIPALIPVYDPS 221  
 DB 193 VSLPWQDSQILINPVSH NQPHQIVYDFVNLQUTETOVIAVES 240

## RESULT 2

US-09-252-429-46  
 Sequence 46, Application US/09252229  
 Patient No. 6147192  
 GENERAL INFORMATION:  
 APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.  
 TITLE OF INVENTION: Weight Control Pathway Genes and Uses  
 NUMBER OF INVENTION: Thetefor  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: LAHIVE & COFFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09252429  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/997,340  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Silver1, Jean M.  
 REGISTRATION NUMBER: 39,030  
 REFERENCE/DOCKET NUMBER: MNT-005CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)227-5941  
 INFORMATION FOR SEQ ID NO: 46:  
 SOURCE CHARACTERISTICS:  
 LENGTH: 245 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 US-09-252-429-46

Query Match 24.5%, Score 205, ID 4, Length 245,  
 Host Local Similarity 28.5%, Pred. No. 1,96-25,  
 Matches 65, Conservative 45, Mismatches 94, Indels 44, Gaps 6  
 DB 46 FVAVLGVVLAIPVLAAGHVGZSLIAMPSSLLHCLGSSVILPFFAVCPFAH 75  
 16 FVYVGVVAVLKVTPVLAAGHVGZSLIAMPSSLLHCLGSSVILPFFAVCPFAH 75  
 87 IIYAKMSEGVNCAETILVCLSEPMALIEPOVYIDK 139  
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 140 -----WCFQCOBELY-FDLSLDEITTHRSRRKVPQCH 174  
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 DB 193 VSLPWQDSQILINPVSH NQPHQIVYDFVNLQUTETOVIAVES 240

DB 133 RSTSSASNTETVQELISSSHPTKPTLCCQESNFKORLLDHNSNHLVQIVYVPT 192  
 174 KIPNPSPSPSGNLIHQVSHIIFYDFIIPNFIIPALIPVYDPS 221  
 DB 193 VSLPWQDSQILINPVSH NQPHQIVYDFVNLQUTETOVIAVES 240

## RESULT 3

US-08-897-340-35  
 Sequence 35, Application US/08897340  
 Patient No. 5945306  
 GENERAL INFORMATION:  
 APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R.  
 TITLE OF INVENTION: Weight Control Pathway Genes and Uses  
 NUMBER OF INVENTION: Thetefor  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: LAHIVE & COFFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08897340  
 FILING DATE:  
 CLASSIFICATION: 445  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/715,032  
 FILING DATE: 17-SEP-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Silver1, Jean M.  
 REGISTRATION NUMBER: 39,030  
 REFERENCE/DOCKET NUMBER: MNT-005CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)227-5941  
 INFORMATION FOR SEQ ID NO: 35:  
 SOURCE CHARACTERISTICS:  
 LENGTH: 245 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 US-08-897-340-35

Query Match 22.5%, Score 283, ID 2, Length 245,  
 Host Local Similarity 30.7%, Pred. No. 4,36-24,  
 Matches 66, Conservative 28, Mismatches 83, Indels 38, Gaps 6  
 DB 46 FVAVLGVVLAIPVLAAGHVGZSLIAMPSSLLHCLGSSVILPFFAVCPFAH 75  
 16 FVYVGVVAVLKVTPVLAAGHVGZSLIAMPSSLLHCLGSSVILPFFAVCPFAH 75  
 87 IIYAKMSEGVNCAETILVCLSEPMALIEPOVYIDK 139  
 DB 76 FNMRFSSGSSCHVSKRLEKYPMPYPSYFYGLVGVSVLNFRLSGSVSSN 142  
 140 -----WCFQCOBELY-FDLSLDEITTHRSRRKVPQCH 174  
 DB 133 RSTSSASNTETVQELISSSHPTKPTLCCQESNFKORLLDHNSNHLVQIVYVPT 192  
 174 KIPNPSPSPSGNLIHQVSHIIFYDFIIPNFIIPALIPVYDPS 221  
 DB 193 VSLPWQDSQILINPVSH NQPHQIVYDFVNLQUTETOVIAVES 240

```
US-09-252-827-45
Sequence: 45, Application US560252129
Patent No.: 6147192
GENERAL INFORMATION
APPLICANT: Olinco, Carlos J. and Erida, Patrick R.
TITLE OF INVENTION: Weight Control Pathway Score and %acc
FILE OF INVENTION: Protocol
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COTTELL, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
FORMAT: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentele Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09-09-252-827-42*
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08-08-75-11
FILING DATE:
ALTERNATE NAME: INFORMATION
NAME: SUOVELI, JOON M.
REGISTRATION NUMBER: 39,034
REFERENCE/CORRECT NUMBER: KRI-005CP
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
LOCAL KEY: lipid
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-252-829-45
Gcctg Match: 22-58; Start: 284; Len: 4; Length: 245;
First Local Similarity: 40-78; End: 4,46-24;
Matches: 60; Conservative: 28; Mismatches: 83; Indels: 38; Gaps: 6.
UY 45 EVAVVLEHVHV-TROCHVCSFAISENNKVCYAYE--SEVP-AHV 89
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UY 1 - - - - - I I I I I I I I I I I I I I I I I I I I I I
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RESULT 5
US-09-198-270-4
Sequence: 4 APPLICATION 09-09-198-270
Patent No.: 6426404
GENERAL INFORMATION
APPLICANT: NAKATA, MOTOMI
APPLICANT: YASITA, HIROYASU
APPLICANT: OKUMURA, KI
```

[illegible]

[illegible]

SOFTWARE: PatentIn Ver. 2.1



```

1  APPLICANT: Xu, Qunli
2  TITLE OF INVENTION: BAX Inhibitor Proteins
3  NUMBER OF SEQUENCES: 16
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Campbell & Flores
6  STREET: 4470 La Jolla Village Drive, Suite 700
7  CITY: San Diego
8  STATE: California
9  COUNTRY: United States
10 ZIP: 92122
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: floppy disk
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patent to Release #1.0, Version #1.25
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08,818,514
17 FILING DATE:
18 CLASSIFICATION: 445
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Campbell, Cathryn A.
21 REGISTRATION NUMBER: 41,815
22 REFERENCE/DOCKET NUMBER: P-LJ 2446
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (619) 535-9001
25 TELEFAX: (619) 535-8949
26 INFORMATION FOR SEQ ID NO: 6:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 450 amino acids
29 TYPE: amino acid
30 TOPOLOGY: linear
31 US 08-818-514-6
32
33 Query Match: 10 34: Score 140; DB 2: Length 450;
34 Best Local Similarity: 42.28; Pred. No. 2, 26-06;
35 Matches: 28; Conservation: 12; Mismatches: 37; Gaps: 10; Gaps: 3;
36
37
38 14 PASATAAPLEPPR-----PELPVTSPPGAVGIEVILGVPPTPGHVEPSPGATSIK 66
39 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
40 4 POKSVNIMDLERDPEIKSTGGYLSVSESPHVCYDLINVLINCHSGHGLALMWA 63
41 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
42
43 67 NKKWT-CPYGPAVLPSTGVPAIVAKR 92
44 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
45 64 SSKTEPEGRE--KWEPPKVSILIK 88
46 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
46
47 RESULT 14
48 US-09-944A-6
49 Sequence 6, Application US/09115944A
50 Patent No. 6130417
51 GENERAL INFORMATION:
52 APPLICANT: Xu, Qunli
53 ADDRESSEE: Xu, Qunli
54 TITLE OF INVENTION: BAX Inhibitor Proteins
55 NUMBER OF SEQUENCES: 16
56 CORRESPONDENCE ADDRESS:
57 ADDRESSEE: Campbell & Flores LLP
58 STREET: 4470 La Jolla Village Drive, Suite 700
59 CITY: San Diego
60 STATE: California
61 COUNTRY: United States
62 ZIP: 92122
63 COMPUTER READABLE FORM:
64 MEDIUM TYPE: floppy disk
65 OPERATING SYSTEM: PC-DOS/MS-DOS
66 SOFTWARE: Patent to Release #1.0, Version #1.25
67 CURRENT APPLICATION DATA:
68 APPLICATION NUMBER: US/09/115,944A
69 FILING DATE:
70 CLASSIFICATION: 445
71 PRIOR APPLICATION DATA:
72 APPLICATION NUMBER: US 08/818,514

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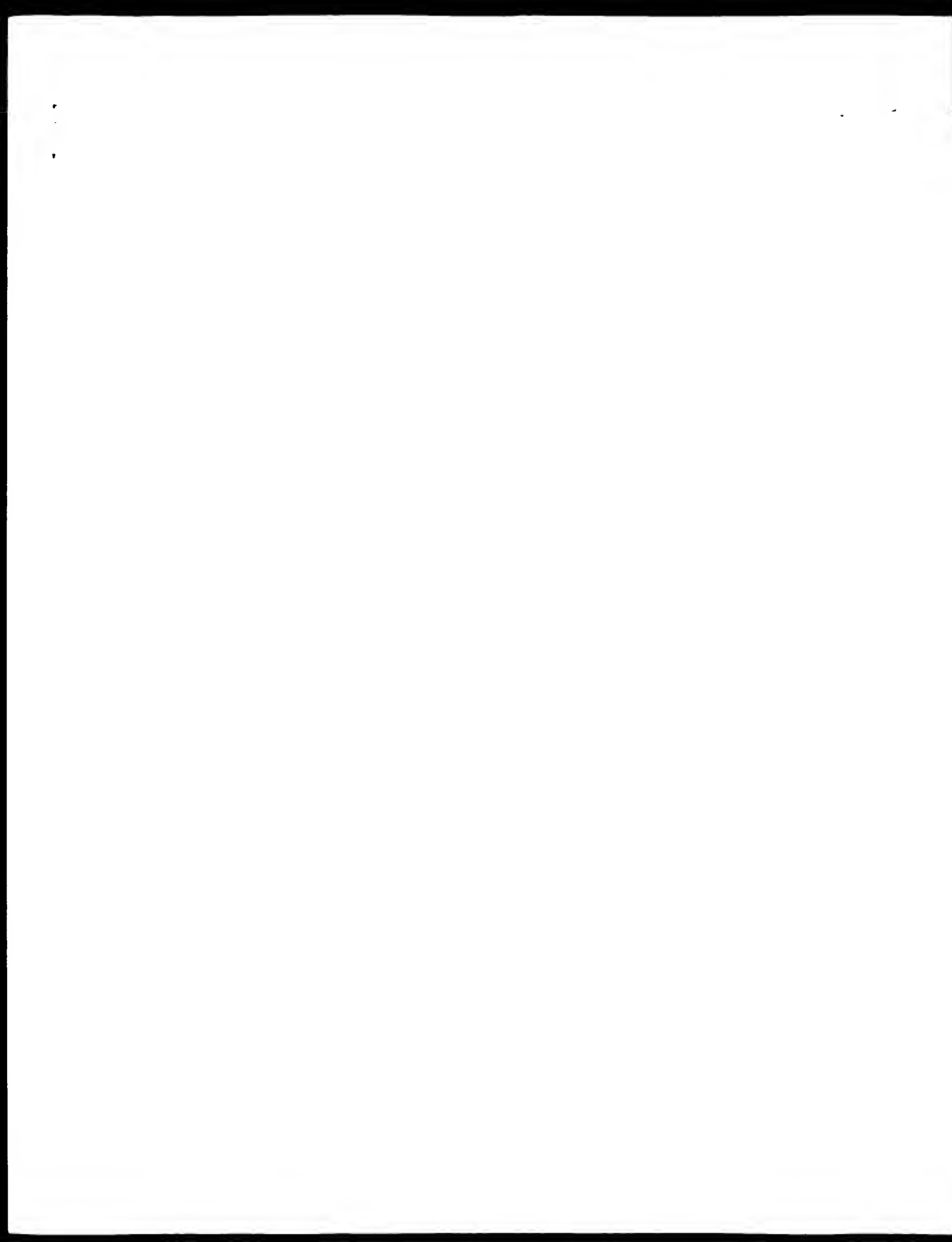
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1  FILING DATE: 14-MAR-1997
2  ATTORNEY/AGENT INFORMATION:
3  NAME: Campbell, Cathryn A.
4  REGISTRATION NUMBER: 41,815
5  REFERENCE/DOCKET NUMBER: P-LJ 4209
6  TELECOMMUNICATION INFORMATION:
7  TELEPHONE: (619) 535-9001
8  TELEFAX: (619) 535-8949
9  INFORMATION FOR SEQ ID NO: 6:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 450 amino acids
12 TYPE: amino acid
13 TOPOLOGY: linear
14 US-09-115-944A-6
15
16 Query Match: 10 34: Score 140; DB 4: Length 450;
17 Best Local Similarity: 32.28; Pred. No. 2, 26-06;
18 Matches: 28; Conservation: 12; Mismatches: 37; Gaps: 10; Gaps: 3;
19
20
21 14 PASATAAPLEPPR-----PELPVTSPPGAVGIEVILGVPPTPGHVEPSPGATSIK 66
22 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
23 4 POKSVNIMDLERDPEIKSTGGYLSVSESPHVCYDLINVLINCHSGHGLALMWA 63
24 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
25
26 67 NKKWT-CPYGPAVLPSTGVPAIVAKR 92
27 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
28 64 SSKTEPEGRE--KWEPPKVSILIK 88
29 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
30
31 RESULT 14
32 US-09-230-196-5
33 Sequence 7, Application US/09230196
34 Patent No. 6307045
35 GENERAL INFORMATION:
36 APPLICANT: Rauscher III, Frank J.
37 ADDRESSEE: Jensen, David E.
38 TITLE OF INVENTION: BACAL Associated Proteins (BAP-1) and
39 TITLE OF INVENTION: Uses Therefor
40 NUMBER OF SEQUENCES: 47
41 CORRESPONDENCE ADDRESS:
42 ADDRESSEE: Howson and Howson
43 STREET: Spring House Corporate Ctr., PO Box 457
44 CITY: Spring House
45 STATE: Pennsylvania
46 COUNTRY: U.S.A.
47 ZIP: 15477
48 COMPUTER READABLE FORM:
49 MEDIUM TYPE: floppy disk
50 OPERATING SYSTEM: PC-DOS/MS-DOS
51 SOFTWARE: Patent to Release #1.0, Version #1.40
52 CURRENT APPLICATION DATA:
53 APPLICATION NUMBER: US/09/230,196
54 FILING DATE:
55 CLASSIFICATION:
56 PRIOR APPLICATION DATA:
57 APPLICATION NUMBER: US 60/022,997
58 FILING DATE: 02-AUG-1996
59 FURTHER APPLICATION DATA:
60 APPLICATION NUMBER: US 60/7048,109
61 FILING DATE: 19-FEB-1997
62 ATTORNEY/AGENT INFORMATION:
63 NAME: Bak, Mary E.
64 REGISTRATION NUMBER: 41,215
65 REFERENCE/DOCKET NUMBER: WST64805A
66 TELECOMMUNICATION INFORMATION:
67 TELEPHONE: 215-540 9200
68 TELEFAX: 215-540-5818
69 INFORMATION FOR SEQ ID NO: 5:
70 SEQUENCE CHARACTERISTICS:
71 LENGTH: 100 amino acids
72 TYPE: amino acid
73 STRANDEDNESS:
74 TOPOLOGY: unknown

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[illegible]

O7	6) LKNNKKCPBPACAVILISEQVPATDARK-----MSEYKNNAE-----	102
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E8	8) LSSSPKPCAGCSIVKPDPVPRNCKRKEIIAQLGYCNESKGABOLTHGLYLHINKP	140
O9	103 -----CDTLVCESEBRARIRTKOQYID-----KYGIJOLFETPAKV	140
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O9	141 CFFGORELYEDSLDLHCITHTHSER--RRRVFPLIK	174
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L6	201 VWSGPBKQSVGTLLBSFTSAHI STCYANASTSTSRP	246







[illegible]

A.M. locale type RNA  
A.bssides: 1-518 -0812  
Accession reference: DDBJ/AB046981  
Comment: This protein is a member of the TcdB toxin family  
Cognate:  
Accession: A11P  
A.Mut position: 67-117  
Alignments: 151 total alignments; 100% identity  
Superfamily: 147 transmembrane proteins; PINT: typical homology  
Keywords: coiled coil; toxins

Query Match 11.4% Score 14.6 E=0.4 Length 518.  
Best Local Similarity 25.4% Posed No. items 25  
Methods 48: Conserved 40: Missed 57: Indels 94: Gaps 72

CY 1-3 ALASATMAI EKKKPPPIIVISIAFAVTEFVIHGFVEVTEGAEVSTSLATSIKNKW + 70  
| | | | | | | | | | | | | | | | | |  
LB 11 ASASAIAPAIENLQ--- --VASDSEVETIKFEVLEIGENTKAFL - IHWV 58

[illegible]

A111161	A novel member of the EAF family of putative signal transduction proteins	1				
A161076	Accession number: 156498, MIM:361290-2, EMBL:354021	1				
A160880	Accession: 588467	1				
A151805	Status: nucleic acid sequence not shown	1				
A160616	Molecular type: mRNA	1				
A160505	Accession: 154135-5817	1				
A160505	Cross-references: EMBL:148509; NID:975557; F11N:AAA01051; F11N:975558	1				
A160505	Experimental source: Tissue-type: fetal brain	1				
A160505	Comments:	1				
A160505	Accession: CAP-1	1				
A160505	Superfamily: Gdn receptor-associated protein (GAP-1) RING finger homology	1				
A160505	Keywords: homodimer; signal transduction; zinc finger	1				
A160505	149-97/Domain: RING finger homology - RING	1				
Query Match	11.4%	Score: 142.1	Id: 27	Length: 142		
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QY 5 LKSDSGKAPASATAAPALPPPELPLVSLAVLPLHQPVLQGHVCPSTALS 64  
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 QY 46 LKNNWQWQWYNAVLYSLVAVLAVAKK MSEEYKNCALDQILVLTSMHAK 116  
 DB 81 LKSSSKFATACQSLVYKVLKPLNFTPLAMQVCPHSHQVA LKCHLAVEL 117  
 QY 112 LK LKNNWQWQWYNAVLYSLVAVLAVAKK MSEEYKNCALDQILVLTSMHAK 116  
 DB 146 LKNNWQWQWYNAVLYSLVAVLAVAKK MSEEYKNCALDQILVLTSMHAK 116

## RESULT 9

149272  
 C:G40 receptor associated factor 1 - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 15-Mar-1996 #sequence\_revision 15 Mar-1996 #text\_change 18-Aug-2000  
 C:Accession: 149272  
 C:Chem: G: Cleary, A.M.; Ye, E.S.; Hong, D.L.; Lederman, S.; Baltimore, D.  
 Science 267, 1494-1498, 1995  
 A>Title: Involvement of CRAF1, a relative of TRAF, in G40 signaling.  
 A:Reference number: A55600; MUID:95184010; PMID:7533327  
 A:Accession: 149272  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-67, 88-93  
 A:Cross-references: EMBL:021950; NID:q719292; PIDD:AMC52175.1; PIR:q719293  
 C:Keywords: CRAP1  
 C:Superfamily: G40 receptor associated protein GAP 1, RING finger homology  
 C:Keywords: zinc finger  
 F:44-96/Domain: RING finger homology <RNG>

Query Match 11.38; Score 142; DB 2; Length 567;  
 Best local similarity 24.28; Pred. No. 0.00043;  
 Matches 45; Conservative 22; Mismatches 73; Indels 46; Gaps 4;

QY 35 FPGACVLEVLHQPVRTRCHVPCSTATSLKNNKWTGVCAYLSEGVDAIVAKK-- 92  
 DB 50 YPPECPVLYCNFTGDSHPPESMAALSSSLKTAQCESLLEKVFETNTEPQ 103  
 QY 93 MKSEYKNCALDQILVLTSMHAK MSEEYKNCALDQILVLTSMHAK 120  
 DB 110 LKNNWQWQWYNAVLYSLVAVLAVAKK MSEEYKNCALDQILVLTSMHAK 116  
 QY 121 KYLDLEETAAKVCPCQDELYEDSLDQITIHRSK--RPV 168  
 DB 170 KYEALGSHKSGVPMKIKQKHDLICPVVVSQPHKSGVQLLSELSAHLSEVNAVS 229  
 QY 169 FPLGR 174  
 DB 240 TSPKR 235

## RESULT 10

139702  
 C:Probable peroxisome assembly protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 02-Sep-2000  
 C:Accession: 139702  
 R:Wood, V.; Skelton, J.; Chertkov, G.M.; Rajandream, M.A.; Barrell, B.G.,  
 submitted to the EMBL Data Library, July 1999  
 A:Reference number: 221875  
 A:Accession: 139702  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-306 <MO>  
 A:Cross-references: EMBL:AL109652; PIDD:CAU51769.1; GSPDB:GN00067  
 C:Experimental source: strain 972h-; cosmid c17A3  
 C:Keywords:  
 A:Gene: p1037  
 A:Map position: 2

A:Accession: 139702  
 C:Superfamily: RING finger homology  
 F:44-96/Domain: RING finger homology <RNG>

Query Match 10.98; Score 137.5; DB 2; Length 306;  
 Best local similarity 49.48; Pred. No. 0.00043;  
 Matches 24; Conservative 11; Mismatches 15; Indels 11; Gaps 2;

QY 22 FPGACVLEVLHQPVRTRCHVPCSTATSLKNNKWTGVCAYLSEGVDAIVAKK 92  
 DB 50 YPPECPVLYCNFTGDSHPPESMAALSSSLKTAQCESLLEKVFETNTEPQ 103  
 QY 93 MKSEYKNCALDQILVLTSMHAK MSEEYKNCALDQILVLTSMHAK 120  
 DB 110 LKNNWQWQWYNAVLYSLVAVLAVAKK MSEEYKNCALDQILVLTSMHAK 116  
 QY 121 KYLDLEETAAKVCPCQDELYEDSLDQITIHRSK--RPV 168  
 DB 170 KYEALGSHKSGVPMKIKQKHDLICPVVVSQPHKSGVQLLSELSAHLSEVNAVS 229  
 QY 169 FPLGR 174  
 DB 240 TSPKR 235

## RESULT 11

A33754  
 C:recombination activating protein 1 - human  
 C:Species: Homo sapiens (man)  
 C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 05-Nov-1999  
 C:Accession: A33754  
 C:Chem: R.G.; Gertinger, M.A.; Baltimore, D.  
 Cell 59, 1045-1048, 1989  
 A>Title: The V(D)J recombination activating gene, RAG-1.  
 A:Reference number: A33754; MUID:9009604; PMID:2598259  
 A:Accession: A33754  
 A:Molecule type: mRNA  
 A:Residues: 1-1043 <SCA>  
 A:Cross-references: M29474; NID:q190845; PIR:AA09248.1; PIR:q190843  
 C:Keywords:  
 C:Superfamily: RAG1  
 A:Cross-references: GDB:120344; OMIM:179615  
 A:Map position: 11p13-11p13  
 C:Superfamily: RING finger homology  
 C:Keywords: DNA binding; zinc finger  
 F:289-337/Domain: RING finger homology <RNG>

Query Match 10.78; Score 134.5; DB 2; Length 1043;  
 Best local similarity 44.58; Pred. No. 0.0025;  
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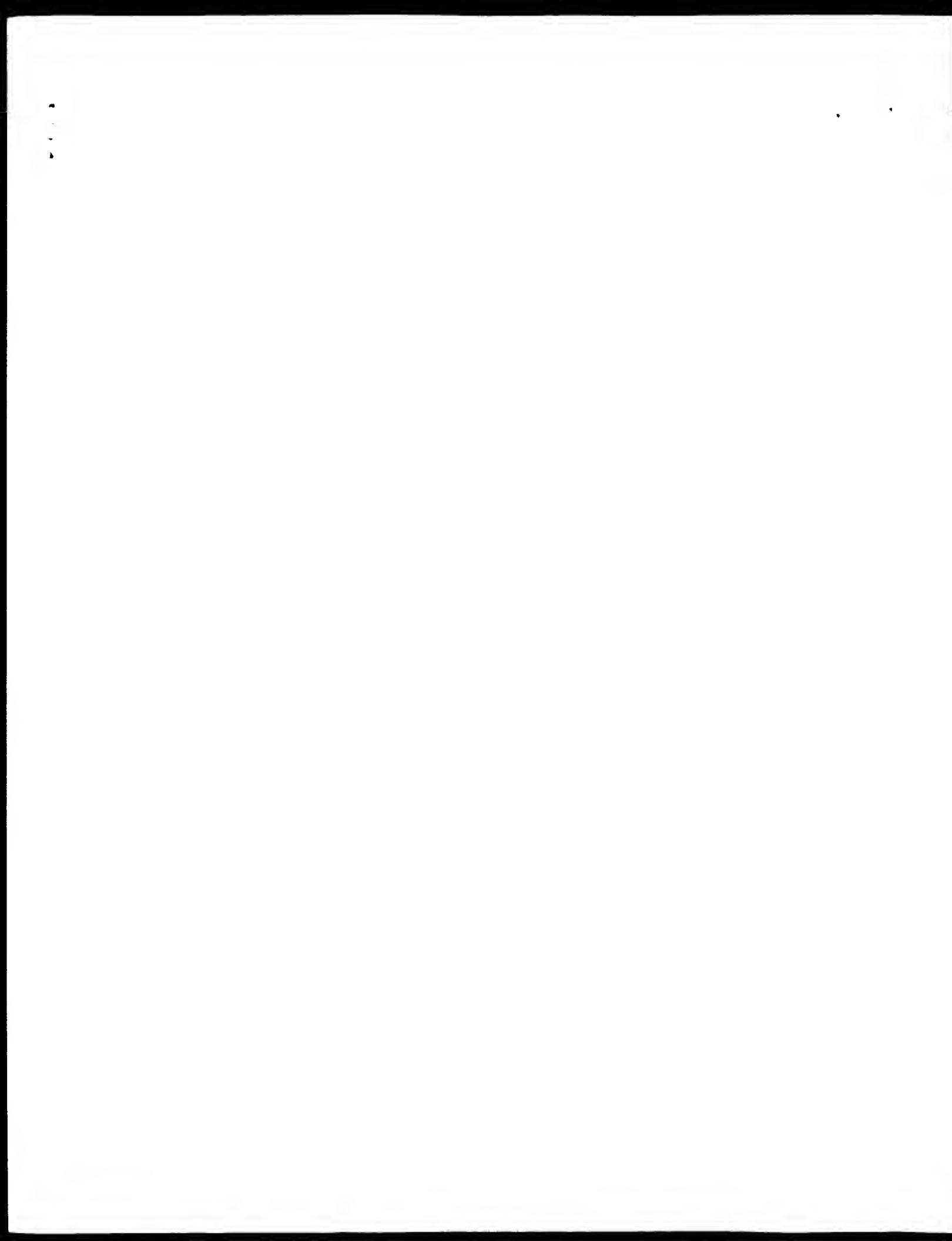
QY 28 PELPISDCAVLEVLHQPVRTRCHVPCSTATSLKNNKWTGVCAYLSEGVDAIVAKK 85  
 DB 284 PEHPKSTSDQICELLADPVRTRCHVPCSTATSLKNNKWTGVCAYLSEGVDAIVAKK 343  
 QY 86 ATDAKKEKSEYKNCALDQILVLTSMHAK MSEEYKNCALDQILVLTSMHAK 120  
 DB 144 VKSFLSVNSIMVAVLAVLAVAKK MSEEYKNCALDQILVLTSMHAK 120

## RESULT 12

151055  
 C:recombination activating protein - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)  
 C>Date: 15-Sep-1996 #sequence\_revision 15-Sep-1996 #text\_change 21-Jul-2009  
 C:Accession: 151055  
 R:Hamson, J.D.; Kaattari, S.L.;  
 Immunogenetics 42, 188-195, 1995  
 A>Title: The recombination activating gene 1 (RAG1) of rainbow trout (Oncorhynchus mykiss)  
 A:Reference number: 151055; MUID:95369845; PMID:7642230  
 A:Accession: 151055  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1073 <MAN>  
 A:Cross-references: EMBL:U15663; NID:q59817; PIDD:AA08281.1; PIR:q558918  
 C:Keywords: RAG-1  
 A:Superfamily: RING finger homology  
 F:44-96/Domain: RING finger homology <RNG>





# us-09-998-667-1

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

us-09-998-667-1 Search time: 23 Seconds  
(without alignment)

418,370 Million cell updates/sec

Perfect Score: 1257  
Sequence: MSVSSTFSSKSAASAIAR.....LRVLRSLLEYSNNTI 242

Scoring Table: HUSUM62  
Gap: 10.0, Expect: 0.5

Search: 112892 seqs, 41476424 residues

Total number of hits satisfying chosen parameters: 112892

Minimum hit seq length: 9

Maximum DB seq length: 200000000

Post processing: Minimum Match: 0.9  
Maximum Match: 100%

Database: SwissProt\_40\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	454.5	28.2	231_MOUSE	Q9426 mouse muscle
2	449	27.8	231_MOUSE	Q9426 mouse muscle
3	447	11.7	231_MOUSE	Q9426 mouse muscle
4	445.5	11.7	231_MOUSE	Q9426 mouse muscle
5	444.5	11.5	231_MOUSE	Q9426 mouse muscle
6	443	11.4	231_MOUSE	Q9426 mouse muscle
7	442	11.3	231_MOUSE	Q9426 mouse muscle
8	442	11.3	231_MOUSE	Q9426 mouse muscle
9	442	11.3	231_MOUSE	Q9426 mouse muscle
10	442	11.3	231_MOUSE	Q9426 mouse muscle
11	442	11.3	231_MOUSE	Q9426 mouse muscle
12	442	11.3	231_MOUSE	Q9426 mouse muscle
13	442	11.3	231_MOUSE	Q9426 mouse muscle
14	442	11.3	231_MOUSE	Q9426 mouse muscle
15	442	11.3	231_MOUSE	Q9426 mouse muscle
16	442	11.3	231_MOUSE	Q9426 mouse muscle
17	442	11.3	231_MOUSE	Q9426 mouse muscle
18	442	11.3	231_MOUSE	Q9426 mouse muscle
19	442	11.3	231_MOUSE	Q9426 mouse muscle
20	442	11.3	231_MOUSE	Q9426 mouse muscle
21	442	11.3	231_MOUSE	Q9426 mouse muscle
22	442	11.3	231_MOUSE	Q9426 mouse muscle
23	442	11.3	231_MOUSE	Q9426 mouse muscle
24	442	11.3	231_MOUSE	Q9426 mouse muscle
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27	442	11.3	231_MOUSE	Q9426 mouse muscle
28	442	11.3	231_MOUSE	Q9426 mouse muscle
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30	442	11.3	231_MOUSE	Q9426 mouse muscle
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34	442	11.3	231_MOUSE	Q9426 mouse muscle
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36	442	11.3	231_MOUSE	Q9426 mouse muscle
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38	442	11.3	231_MOUSE	Q9426 mouse muscle
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42	442	11.3	231_MOUSE	Q9426 mouse muscle
43	442	11.3	231_MOUSE	Q9426 mouse muscle
44	442	11.3	231_MOUSE	Q9426 mouse muscle
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44	113	9.0	1812	1	BRN1_MOUSE	P4874 mouse muscle
45	112.5	8.9	1812	1	BRN1_MOUSE	P4874 mouse muscle
46	112.5	8.9	1812	1	BRN1_MOUSE	P4874 mouse muscle
47	112.5	8.9	1812	1	BRN1_MOUSE	P4874 mouse muscle
48	111.5	8.9	1812	1	BRN1_MOUSE	P4874 mouse muscle
49	111.5	8.9	1812	1	BRN1_MOUSE	P4874 mouse muscle
40	111	8.8	1812	1	BRN1_MOUSE	P4874 mouse muscle
41	110.5	8.8	1812	1	BRN1_MOUSE	P4874 mouse muscle
42	109.5	8.7	1812	1	BRN1_MOUSE	P4874 mouse muscle
43	109.5	8.7	1812	1	BRN1_MOUSE	P4874 mouse muscle
44	109	8.7	1812	1	BRN1_MOUSE	P4874 mouse muscle
45	108.5	8.6	1812	1	BRN1_MOUSE	P4874 mouse muscle

## ALIGNMENTS

46	112.5	8.9	1812	1	BRN1_MOUSE	P4874 mouse muscle
47	112.5	8.9	1812	1	BRN1_MOUSE	P4874 mouse muscle
48	111.5	8.9	1812	1	BRN1_MOUSE	P4874 mouse muscle
49	111.5	8.9	1812	1	BRN1_MOUSE	P4874 mouse muscle
40	111	8.8	1812	1	BRN1_MOUSE	P4874 mouse muscle
41	110.5	8.8	1812	1	BRN1_MOUSE	P4874 mouse muscle
42	109.5	8.7	1812	1	BRN1_MOUSE	P4874 mouse muscle
43	109.5	8.7	1812	1	BRN1_MOUSE	P4874 mouse muscle
44	109	8.7	1812	1	BRN1_MOUSE	P4874 mouse muscle
45	108.5	8.6	1812	1	BRN1_MOUSE	P4874 mouse muscle









198. M. J. D. McCall, 1890, 6, 59. R. H. L. 3.

ASSOCIATED FACTORS (POTENTIAL):





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E1 DUA_RINR 421 476 NBD
E2 METAL 633 643 DIVALENT METAL ION (BY SIMILARITY)
E3 METAL 743 743 DIVALENT METAL ION (BY SIMILARITY)
E4 ACT_SITE 997 997 BY SIMILARITY
E5 SEQUENCE 1073 AA: 12,044 MW: 2683080.870985 CR:64.

Query Match
Best local similarity: 28.0%, Fred. No. 0.00029
Matches: 42, Conservative: 13, Mismatches: 41, Indels: 44, Gaps: 4

DY 18 TAALEBRKRPPEPV---TSFEAVTLPVHGVHICSHVPESTAIISKNNKTCY 74
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DY 76 CAAVLPSCGVATDVAKKMKSEYKNCACDLVLVLSNPAPHPQCQYIKYCPDCELE 144
DY 448 C---LPCGPAULTAAK-----DPLGVHNS 470
DY 145 IAAQVTPVPEFLYFOSILLGTHHPSE 164
DY 371 LPLCPRESGCGVAVLSPFACGLGHLE 400

RESULT 11
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DT 01-APR-1990 (Rel. 14, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tripartite motif protein 40 (Down regulatory protein of Interleukin 2 receptor).
GN TRIM30 OR PPT1 OR RPT-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Eumetazoa; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DX NCBI_Taxid 10090:
RN [1]
RP SEQUENCE FROM N A (ISOFORM ALPHA).
RX MEDLINE: 88190142; PubMed: 2965815;
RA Palanca P., Schwartz J., Singh P.P., Kong Q.-T., Murphy E.,
RA Anderson Y., Sheng F.-Y.W., Singh P., Johnson K.A., Guadagnoli S.M.,
RA Dutteer T., Blatner F., Cantor H.;
*PPT1, an intracellular protein from helper/inducer T cells that
*regulates gene expression of interleukin 2 receptor and human
*immunodeficiency virus type 1.
RT Proc Natl Acad Sci U S A 85:2744-2747(1988)
RN [2]
RP EPRATUM
RA Palanca P., Schwartz J., Singh P.P., Kong Q.-T., Murphy E.,
RA Anderson Y., Sheng F.-Y.W., Singh P., Johnson K.A., Guadagnoli S.M.,
RA Dutteer T., Blatner F., Cantor H.;
*PPT1, an intracellular protein from helper/inducer T cells that
*regulates gene expression of interleukin 2 receptor and human
*immunodeficiency virus type 1.
RT Proc Natl Acad Sci U S A 85:2744-2747(1988)
RN [3]
RP SEQUENCE FROM N A (ISOFORM ALPHA AND BETA).
RX MEDLINE: 21241161; PubMed: 11331580;
RA Roychowdhury A., Merzani C., Panecchia A., Morris G., Gatto S., Jui J.,
RA Kikawell D., Zandari E., Messali S., Calandra S., Guftanti A.,
RA Minucci S., Pelicci P.G., Rallabio A.;
*The tripartite motif family identifies cell compartments.
RT EMBO J. 20:2140-2151(2001).
RN [4]
RP SEQUENCE FROM N A (ISOFORM ALPHA).
RA Strassberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/CCRC databases
*FUNCTION: TRANS-ACTING FACTOR THAT REGULATES GENE EXPRESSION OF
INTERLEUKIN 2 RECEPTOR ALPHA CHAIN AND OF HUMAN IMMUNODEFICIENCY
VIRUS TYPE 1. MAY AFFECT IL2-ALPHA AND HIV-1 EXPRESSION THROUGH
CIS-ACTING NEGATIVE REGULATORY ELEMENTS OR THROUGH COMPETITION
WITH PROTEINS THAT BIND TO ENHANCER OR ACTIVATOR SEQUENCES.
*SUBCELLULAR LOCATION: Nucleus.
*ALTERNATIVE PRODUCTS: 2 isoforms: Alpha (shown here) and Beta; are
produced by alternative splicing.

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CC -1- SIMILARITY: CONTAINS 1 KINZ-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 R-BOX-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
CC -1- CAUTION: Rel.1 sequence differs from that shown due to a
frame shift in position 419.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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modified and this statement is not removed, usage by and for commercial
entities requires a license agreement (See http://www.isb.sib.ch/announcements
or send an email to license@isb.sib.ch).
CC
CC EMBL: J03776; AAA40073.1; ALT_FRAME.
CC EMBL: AF220014; AAG54468.1;
CC EMBL: AF220015; AAG54469.1;
CC EMBL: AF220016; AAG54470.1; ALT_INIT.
CC EMBL: H6005447; AAI05447.1;
CC PIR: A40891; A30891.
CC BSSP: P28990; ICHC.
CC MGI: MGI:98178; Trm40.
CC InterPro: IPR001870; Gamma_carboxylase.
CC InterPro: IPR004878; SPRY_domain.
CC InterPro: IPR003877; SPRY_receptor.
CC InterPro: IPR003151; Znf_Box.
CC InterPro: IPR001841; Znf_Tfnq.
CC Pfam: PF00097; Zf-G3HC4.1.
CC Pfam: PF06422; SPRY.1.
CC Pfam: PF03443; Zf_B_Box.1.
CC PRINTS: PR01406; BRX2NEINGER.
CC SMART: SM00336; BRX.1.
CC SMART: SM00184; RING.1.
CC SMART: SM00449; SPRY.1.
CC PROSITE: PS50119; ZF-BBOX.1.
CC PROSITE: PS50118; ZF-RING.1.
CC PROSITE: PS50089; ZF-RING_2.1.
CC K1 transcription regulation: DNA-binding; Trans-acting factor;
K2 zinc-finger; Nucleic protein; Alternative splicing.
CC K3 RING.1.
CC K4 RING-TYPE.
CC K5 RING-TYPE.
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15 JUN 2002 (ref. 41, last annotation update)  
 16 Postrept. from repair protein RAD18  
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 20 Saccharomycetiales; Saccharomycetaceae; Saccharomycetes.  
 21 NCBI\_LinkID:4932;  
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10 SIMILARITY: CONTAINS 1 SPRY DOMAIN.

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EMBL: 009629; AAA9431.1;  
EMBL: AF010517; BAB6330.1;  
GenBank: F2961296; IRIM26;  
MIM: 609830;  
InterPro: IPR001870; Gamma\_carboxylase;  
InterPro: IPR004878; SPRY\_dom1n;  
InterPro: IPR004877; SPRY\_receptor;  
InterPro: IPR00315; Znf\_Box;  
InterPro: IPR001841; Znf\_Box;  
InterPro: IPR00997; Znf\_Box; 1;  
InterPro: IPR00622; SPRY; 1;  
InterPro: IPR00643; Znf\_Box; 1;  
InterPro: IPR01406; BboxZNFINTER;  
SMART: SM00346; BBOX; 1;  
SMART: SM00184; RING; 1;  
SMART: SM00449; SPRY; 1;  
ProSITE: PS0119; ZF\_BOX; 1;  
ProSITE: PS00516; ZF\_RING\_1; FALSE\_NEG;  
ProSITE: PS0089; ZF\_RING\_2; 1;  
Kw Zinc-finger; Coiled coil;  
F1 ZN\_RING 16 57 RING-TYPE;  
F1 ZN\_RING 97 138 B\_BOX-TYPE;  
F1 DOMAIN 188 227 COILED COIL (POTENTIAL);  
F1 DOMAIN 465 539 SPRY;  
F1 DOMAIN 488 490 POLY-GLU;  
F1 DOMAIN 422 432 POLY-GLU;  
SEQUENCE 639 AA: 62165 MM: 842A71C41F2E2448 GC664;

Query Match 10.0% Score 126; 108 1; Length 539;

Best local similarity 26.7% Prot. NO. 0.00072;

Matches 41; conservative 40; Mismatches 58; Indels 44; Gaps 9;

16 SATAKATERRRPPET PVSSTPAVCI FVHQVPTGQIVCPSCG--ATSEKNNKWTCP 74  
11 1111 11 1111 11 11111111 11 11111111 11 11  
4 SAPLRSLER-----VFGSTGIDYLRPPVITAGHWFCRSCTTIWPTISGRVCP 54  
11  
74 YKRAVPSFNV-PATVA-----KPMK-SFYKMTAP-TLLVLSFMKAHTRGQRYIY 125  
11  
55 LCKKPKKENTRPWALASIVFNTERPKVKGQAPGE-----VTEQQAQKLGEMREK 108  
11  
126 YGPGQELFEITAKRVCVFGQR-----ELYEDSLIDGCTFNIR 162  
11  
109 ---LHYV-EIAGKILAVWCKRSRHRHILAVIMKKAQVIREKILNLSLTKR 158

Search completed: June 18, 2003, 17:27:51

Job time: 1:25, secs



CompuVer version 5.1.6  
(c) 1994 - 2003 CompuVer Ltd

Copyright (c) 1994 - 2003 Computer Ltd

1M protein protein search, using sw model

June 18, 2003, 17:27:22 : Search time 89 seconds  
(without alignments)  
507.527 million reads

597.537 Million (€12)

597.537 Million cell updates/s...

$$1 - (2.7) - 8.66 - 1.51$$

Sequencia: I MÖSVLSTIDOKSÄi ÅSÄi AR. . . . . LIKRV.LÖKSLLT.VNHSNI i 212

SECRETING TABLE  
 FILE(S) M6,2  
 (TABLES 111,0), (TABLES 111,0)

Chapter 11.1 : Chapter 11.1

671580 seqs, 206647115 residues

Total number of hits satisfying chosen parameters: 671580

Maximum lbs seed length: 20000(100)

Maximum life span: 2000000000

Post processing. Minimum Match: 0.8  
Maximum Match: 1.000

List and List 45 Summaries

Lat. 40.45 N

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1:  SP_Removal: *
2:  SP_Archive: *
3:  SP_Backup: *
4:  SP_Fault: *
5:  SP_Human: *
6:  SP_LiveRecreate: *
7:  SP_Mammal: *
8:  SP_Mine: *
9:  SP_Organelle: *
10: SP_Phage: *
11: SP_Plant: *
12: SP_Robot: *
13: SP_Virus: *
14: SP_Vertibrate: *
15: SP_Virus: *
16: SP_Backup: *
17: SP_Archive: *

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pred. No. is the number of results predicted by *ebance* to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Simmons et al.

Result No	Score	Quality Match	Length	DB	ID	Description
1	1.25	100.0	2.2	4	Q08X39	Q08X39 homo sapien
2	1.21	97.4	2.2	4	Q08E08	Q08E08 homo sapien
3	1.197	95.2	2.2	6	Q05K11	Q05K11 macaca fasc
4	1.004	97.8	2.8	11	Q09D86	Q09D86 mus musculus
5	0.76	97.8	1.3	11	Q09D86	Q09D86 mus musculus
6	0.66	26.7	2.7	4	Q06A37	Q06A37 homo sapien
7	0.64	24.1	2.8	11	Q09D86	Q09D86 mus musculus
8	0.59	21.5	2.5	11	Q06D10	Q06D10 mus musculus
9	0.287	22.8	2.5	4	Q08WD3	Q08WD3 homo sapien
10	0.27	27.7	2.5	4	Q04B16	Q04B16 mus musculus
11	0.24	17.9	1.8	11	Q09D86	Q09D86 mus musculus
12	0.11	17.9	2.9	11	Q09D86	Q09D86 mus musculus
13	0.09	16.6	2.9	11	Q09D86	Q09D86 mus musculus
14	0.1	15.2	1.8	4	Q08D19	Q08D19 homo sapien
15	0.07	14.5	1.8	4	Q08D87	Q08D87 homo sapien
16	0.06	14.1	1.7	4	Q08HK2	Q08HK2 homo sapien

17	160.5	12.8	475	5	U01A04	U01A04 diosaphila
18	160.5	12.8	475	5	U01A19	U01A19 diosaphila
19	156.5	12.5	530	11	U70136	U70136 mus musculus
20	155.5	12.4	557	4	U00463	U00463 mus musculus
21	155	12.3	522	4	U00463	U00463 mus musculus
22	152.5	12.1	526	11	U26289	U26289 mus musculus
23	149.5	11.9	463	5	U08Y09	U08Y09 diosaphila
24	148.5	11.8	504	11	U01490	U01490 mus musculus
25	148.5	11.8	558	11	U70191	U70191 mus musculus
26	143.5	11.4	576	11	U70147	U70147 mus musculus
27	142.5	11.3	528	15	U01805	U01805 xenopus laevis
28	141	11.2	545	5	U06V65	U06V65 diosaphila
29	141	11.2	541	5	U06K63	U06K63 diosaphila
30	139.5	11.1	504	5	U03965	U03965 mus musculus
31	137.5	10.9	406	3	U00B00	U00B00 scilla zosterach
32	146.5	10.9	468	11	U01508	U01508 scilla zosterach
33	146	10.8	456	11	U06B82	U06B82 mus musculus
34	145	10.8	447	11	U03F83	U03F83 mus musculus
35	143.5	10.6	447	6	U28463	U28463 mus musculus
36	143	10.6	413	11	U00886	U00886 mus musculus
37	143	10.6	417	4	U07508	U07508 mus musculus
38	143	10.6	417	11	U01568	U01568 mus musculus
39	143	10.6	417	11	U00882	U00882 mus musculus
40	142.5	10.5	561	15	U00885	U00885 mus musculus
41	141.5	10.5	559	5	U01805	U01805 diosaphila
42	141.5	10.5	1479	13	U04001	U04001 diosaphila
43	141	10.4	505	11	U06180	U06180 mus musculus
44	140.5	10.3	1598	4	U00127	U00127 mus musculus
45	140	10.3	425	10	U03944	U03944 diosaphila

# ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED

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RESULT 1
CONSUS 9
ID CUSUS9 PEELIMINARY: 101: 2.2 AA
AC CUSUS9:
01 01-001-2000 (ITEMBL01_15, created)
04 01-001-2000 (ITEMBL01_15, last sequence update)
04 01-001-2000 (ITEMBL01_21, last annotation update)
04 CINA.FL200456.115, clone KAL05627.
05 Homo sapiens (Human).
06 Enkalyoc; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
07 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
08 NC_011410.9606;
09
10 SEQUENCE FROM N.A.
11
12 Watanabe K, Kimoto A, Takaya S, Yaguchi M, Ishino H, et al.
13 Seki Y, Ogasawara M, Nishi Y, Shikihara T, Inakura T,
14 Nakamura Y, Iwata I, Saito S,
15 "Human genome sequencing project."
16 International Gen. group for the Human Genome Project.
17
18 - 15. SIMILARITY. CONTAINS 1 PIRM. THE 21ST PIRM.
19 EMBL: AK000463, BAA1062.1;
20
21 HSSP: F15919; IRSD
22
23 Triclotro; IP060562; FN_Type_11
24
25 InterPro: IP018415; ZIL_F104;
26 Etlag; F00097; Z1-0804_1.
27
28 SMART; SMART059; F12_1.
29
30 SMART; SMART184; F103_1.
31
32 Triclotro; 150018; ZF_F102_1; 1
33 Z1-0804
34
35 SEQUENCE 2.2 AA: 2481 MW: 14199.44 kDa; 17.6% CP04.
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07 158 ITHBSPSPVPTGCGTTCFNNSSGNNIAGGVSCHLGYCELIINLEALAPFV 217
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
08 170 VESHPSPDPKRVVPLDSAMPWQWISYKSNPLQHLHHRKSYLTFVPSIDPEAVQAA 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
09 218 LDRSLLE 224
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10 240 LALSLSE 236
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
090999 PRELIMINARY: PRT: 248 AA.
ID 090999
AC 090999
DE 01-JUN-2001 (TREMURel 17, Created)
DE 01-JUN-2001 (TREMURel 17, Last sequence update)
DE 01-MAR-2002 (TREMURel 20, Last annotation update)
DE 1700045119RIK Protein.
DE 1700045119RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NBI_TaxID=10090;
RN |||
RP SEQUENCE FROM N.A.
RC SRAIN=5786/63; TISSUE=EMBRYONIC STEM CELLS, AND EMBRYO;
RX MEDLINE=21095660; PubMed=11217851;
KA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
KA Atakawa T., Hara A., Fukunishi Y., Kono H., Abuchi T., Fukuda S.,
KA Akawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
KA Saito T., Okazaki Y., Gajothori T., Kono H., Kasukawa T., Saito K.,
KA Kadota K., Matsuda H.A., Ashburner M., Jalcob S., Gashard T.,
KA Fletchman W., Gaslerland T., Gissi T., King H., Kochwa H.,
KA Kuchl J., Lewis S., Matsuo Y., Nikaido T., Hosole A., Goshkenbush J.,
KA Schiml J. M., Stahl J. F., Suzuki K., Tanaka M., Wagner L., Washig T.,
KA Sakai K., Goido T., Furuno M., Aono H., Baldarelli K., Barsh G.,
KA Blake J., Botellid., Bojunga N., Carninci P., de Bonaldo M.F.,
KA Brownstein M. I., Bull T., Fletcher C., Fujita M., Gaitheidi M.,
KA Gustinich S., Hill D., Holman M., Hume D.A., Kaniya M., Lee N.H.,
KA Lyons P., Marchionni J., Mashima J., Mazzarilli J., Mombavets P.,
KA Nordrup P., Rijn B., Ringwald M., Rodriguez L., Savatieri N.,
KA Sasaki H., Sato K., Schenbach G., Soga T., Shibata Y., Storch K.F.,
KA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlock G., Wilming L.,
KA Wynshaw-Boris A., Yoshida K., Yasagawa Y., Kawaji H., Kohlsaki S.,
KA Hayashizaki Y.,
KA "Functional annotation of a full-length mouse cDNA collection."
KA Nature 409:645-646(2001).
CC -1- SIMILARITY: CONTAINS 1 PING-TYPE ZINC FINGER.
DE EMBL: AK006700; BAB24708.1;
DE MGI: MG1:1921514; 1700045119RIK.
DE InterPro: IPR000822; Znf_C2H2.
DE InterPro: IPR001841; Znf_C104.
DE Pfam: PF00997; Zf-C4HC4.1.
DE SMART: SM00184; PINC.1.
DE SMART: SM00155; Znf_C2H2.1.
KW Zinc finger.
SQ
>query Match: 24.18; Score 303; DB 11; Length 248;
>Best Local Similarity: 50.94; Prod No. 4.26 29;
>Matches 72; Conservative 29; Mismatches 90; Indels 42; Gaps 6;

07 35 FDCAVCLEVHLQFVR-TRGCHVFCSCGATSLKNNKWPQPGRAVLSP----GVAVTDV 89
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
08 17 FVCPVQGVKIPVPAAC-KHVPCKKGLSKAKESLHPCRCGNVTRERACVPAVDL 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
09 90 AKPMKSEYKNCANIDTLV-LESPKALIPYKYITIKYG----- 127
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
10 77 FTIMHLPQNCRCQSGVRELHYMRQYKTCGEYQIFGVSTVSFQGSIPSVNSNNEA 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
11 128 -----FLQHLRLAA K-VSPFGVR-ELYEDSLDRITTHRSKRRFVHTVGR 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
12 137 PASANAEVLQEEFENASPDDETFDPLCEFTWMSKORLIDHCNSHRCQAVSVCPDGL 196
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07 175 LITPHEHSSISGNNIAGGVSCHLGYCELIINLEALAPFV 227
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08 197 SLHPWQDPQPTFNVSHLNRHRLHYPVNLGAPVNLGAPVNLGAPVNLGAPVNL 247
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RESULT 8
090999 PRELIMINARY: PRT: 245 AA.
ID 090999
AC 090999
DE 01-JUN-2001 (TREMURel 17, Created)
DE 01-JUN-2001 (TREMURel 17, Last sequence update)
DE 01-MAR-2002 (TREMURel 20, Last annotation update)
DE 2410015A17RIK Protein.
DE 2410015A17RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NBI_TaxID=10090;
RN |||
RP SEQUENCE FROM N.A.
RC SRAIN=5786/63; TISSUE=EMBRYONIC STEM CELLS, AND EMBRYO;
RX MEDLINE=21095660; PubMed=11217851;
KA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
KA Atakawa T., Hara A., Fukunishi Y., Kono H., Abuchi T., Fukuda S.,
KA Atakawa T., Hara A., Fukunishi Y., Kono H., Abuchi T., Fukuda S.,
KA Saito T., Okazaki Y., Gajothori T., Kono H., Kasukawa T., Saito K.,
KA Kadota K., Matsuda H.A., Ashburner M., Jalcob S., Gashard T.,
KA Fletchman W., Gaslerland T., Gissi T., King H., Kochwa H.,
KA Kuchl J., Lewis S., Matsuo Y., Nikaido T., Hosole A., Goshkenbush J.,
KA Schiml J. M., Stahl J. F., Suzuki K., Tanaka M., Wagner L., Washig T.,
KA Sakai K., Goido T., Furuno M., Aono H., Baldarelli K., Barsh G.,
KA Blake J., Botellid., Bojunga N., Carninci P., de Bonaldo M.F.,
KA Brownstein M. I., Bull T., Fletcher C., Fujita M., Gaitheidi M.,
KA Gustinich S., Hill D., Holman M., Hume D.A., Kaniya M., Lee N.H.,
KA Lyons P., Marchionni J., Mashima J., Mazzarilli J., Mombavets P.,
KA Nordrup P., Rijn B., Ringwald M., Rodriguez L., Savatieri N.,
KA Sasaki H., Sato K., Schenbach G., Soga T., Shibata Y., Storch K.F.,
KA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlock G., Wilming L.,
KA Wynshaw-Boris A., Yoshida K., Yasagawa Y., Kawaji H., Kohlsaki S.,
KA Hayashizaki Y.,
KA "Functional annotation of a full-length mouse cDNA collection."
KA Nature 409:645-646(2001).
CC -1- SIMILARITY: CONTAINS 1 PING-TYPE ZINC FINGER.
DE EMBL: AK010486; BAB26977.1;
DE MGI: MG1:1929211; Trif.
DE InterPro: IPR000822; Znf_C2H2.
DE InterPro: IPR001841; Znf_C104.
DE Pfam: PF00997; Zf-C4HC4.1.
DE SMART: SM00184; PINC.2.
DE SMART: SM00155; Znf_C2H2.1.
KW Zinc finger.
SQ
>query Match: 23.98; Score 295; DB 11; Length 245;
>Best Local Similarity: 28.79; Prod No. 4.86 22;
>Matches 65; Conservative 35; Mismatches 86; Indels 44; Gaps 6;

07 35 FDCAVCLEVHLQFVR-TRGCHVFCSCGATSLKNNKWPQPGRAVLSP----GVAVTDV 89
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
08 16 FVCPVQGVKIPVPAAC-KHVPCKKGLSKAKESLHPCRCGNVTRERACVPAVDL 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
09 87 GVAAKMSKSYNNVAF-ITILV-TSEMKALIPYKYITIKYG----- 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
10 76 ENIMKPSG----SCKPSKRIKPYKPKHYSCKKYGQVSVVSNITPNNISQSVSSN 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
11 140 -----VCPQGLRY EQLSLDRITTHRSKRRFVHTVGR 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
12 174 RLITPHEHSSISGNNIAGGVSCHLGYCELIINLEALAPFV 221
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
13 193 SLHPWQDPQPTFNVSHLNRHRLHYPVNLGAPVNLGAPVNLGAPVNLGAPVNL 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 12			
099P02			
ID	099P02	PRELIMINARY	PRT: 209 AA.
AC	099P02		
DI	01-JUN-2001 (TEMBR01: 17, Created)		
DI	01-JUN-2001 (TEMBR01: 17, Last sequence update)		
DI	01-MAR-2002 (TEMBR01: 20, Last annotation update)		
DE	RSD-4.		
OS	PORTS PROTEINOS (P1).		
OC	Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eulioria; Rodentia; Sciurimorphi; Muridae; Murinae; Patton.		
OX	UniProtKB:Q0116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RT	TISSUE-TESTIS;		
RA	Wang L., Gon D., Zhang X.;		
RF	"A rat testis specific gene including a PING finger domain homologous to HSP-4."		
RL	Submitted (01-2001) to the EMBL/GenBank/DDBJ databases		
CC	1. SIMILARITY: CONTAINS 1 PING-TYPE ZINC FINGER.		
DR	EMBL: AF15468; AAK128.1;		
DR	InterPro: IPR000822, Znf_C2H2.		
DR	InterPro: IPR01841, Znf_C1H4.		
DR	Pfam: PF0097; zf-C4HC4.1.		
DR	SMART: SM0184; RING: 1.		
DR	SMART: SM0185; Znf_C2H2: 1.		
RW	Zinc finger.		
SD	SEQUENCE: 209 AA; 24072 MW; 67AAAEAE24CFDB CRR64;		

[illegible]



Job time - 82 seconds

FA Takahashi F., Fujii A., Oshima A., Shioyama A., Kawakami H., Suzuki Y.,  
 KA Saitono S., Nishitani K., Masuda Y., Nagai K., Igarashi T.,  
 FI "Neo" human cDNA sequencing project.",  
 KL Submitted (v1.2.2017) to the EMBL/GenBank/DDBJ databases.  
 EMBL: AK057201; BAB71580.1; ...  
 LR 1000-Pro: 1180002950; 30587416  
 LR 1000-Pro: 118000452; Znt\_2FH2.  
 LR 1000-Pro: 18028639; 01M: 1.  
 LR SMART, SMO0455; Znt\_2FH2; ...  
 LR PROSITE: PS01057; ZINC\_FINGER\_C2H2\_2: 1.  
 LR CNA Database; Zntc 11048;  
 SC SEQUIN-E; 148 AA; 14378 MW; 57066ED1AB8719630 (R064;

Query Match	Score	DB	Length
Host Local Similarity	31.4%	Pred. No. 6, 8e-12;	
Matches	43	Conservative	17
Mismatches	43	Indels	44
Gaps	4		

[illegible]

## RESELL 15

ID	COMMENT	PRELIMINARY	FILE	184 AA
AP	01 MAY 2000 (TEMPREL_13, Created)			
BT	01 MAY 2000 (TEMPREL_13, Last sequence update)			
DI	01 MAY 2000 (TEMPREL_20, Last annotation update)			
DE	Hydrophobic 21.3 kDa protein (Fragment).			
EN	ORF3441714.			
OS	Homo sapiens (Human).			
OX	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
PN	NP_148102.9606.			
PP	11			
PT	SEQUENCE FROM A			
PT	LISSUE TESTES			
KA	Kocher K., Boyer A., Moses H.W., Gassnerhuber J., Wiemann S., Schmidl D. (1997) 1997) to the EMBL/Genbank/DBP4 databases.			
IK	EMBL: A1145557; U0663712.1; -			
IL	Uncloned: 119000822; 2617282.			
IR	SMART: SM00455; ZNF-282; 1.			
DR	Hydrophobic protein.			
KM	Non-ter			
FI	1			
SC	SEQUENCE	184 AA; 21304 MW; EC6A5644243112128 CRO54;		

Query Match	14.58;	Score	182.5;	DB 4:	Length	183;	
Fast Local Similarity	25.48;	Fold. No.	7, Feb-11;				
Matches	43;	Conservative	26;	Mismatches	67;	Models	3;
						Gaps	1;

[illegible]

Search completed - June 18, 2003. 17:40:39

